

# SEQUENCE LISTING

<110> Saris, Christiaan M.  
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Xia, Min  
Bass, Michael B.  
Craveiro, Roger

<120> Interleukin-1 Receptor Antagonist-Related Molecules and  
Uses Thereof

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<150> 60/170,191

<151> 1999-12-10

<150> 60/188,053

<151> 2000-03-09

<150> 60/194,521

<151> 2000-04-04

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<170> PatentIn Ver. 2.0

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gac cag aag gct cta tac aca aga gat ggc cag ctg ctg gtg gga gat	156
Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val Gly Asp	
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Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Thr Leu Pro Asn	
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cag ctg gag gat gtg aac att gag gaa ctg tac aaa ggt ggt gaa gag 348
Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu
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Leu Glu Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
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Thr Lys Phe Tyr Phe Glu Gln Ser Trp
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caaaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 722

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Gly Leu Asp Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly  
50 55 60

Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln  
65 70 75 80

Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly Glu Glu Ala  
85 90 95

Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala Phe Arg Leu  
100 105 110

Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro  
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35 40 45

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Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly  
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100 105 110

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Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu
115 120 125

ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca gcc cgt 492
Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser Ala Arg
130 135 140

acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga aactgcgttt 542
Thr Lys Phe Tyr Phe Glu Gln Ser Trp
145 150

tagccttgtg cccccaaacc aagctcatcc tgctcagggt ctatggtagg cagaataatg 602

tccccgaaa tatgtccaca tcctaataccc aagatctgtg catatgttac catacatgtc 662

caaagaggtt ttgcaaatgt gattatgtta aggatcttga aatgaggaga caatcctggg 722

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gcaggtgttt ttagaagggtg gaaaagccaa gggaacggat tctcctctag agtctccgga 902

aggaacacag ctcttgacac atggatttca gctcagtgac acccatttca gacttctgac 962

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35 40 45

Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile Gln Gly Gly
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Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro Ser Leu Gln
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 Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro Ala Glu Pro  
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 Tyr Ala Asp Gln Lys Ala Leu Tyr Thr Arg Asp Gly Gln Leu Leu Val  
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 gga gat cct gtt gca gac aac tgc tgt gca gag aag atc tgc ata ctt 249  
 Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu  
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 cct aac aga ggc ttg gcc cgc acc aag gtc ccc att ttc ctg ggg atc 297  
 Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile  
                     65                    70                    75                    80  
 cag gga ggg agc cgc tgc ctg gca tgt gtg gag aca gaa gag ggg cct 345  
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 Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly  
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gaa gag gcc aca cgc ttc acc ttc ttc cag agc agc tca ggc tcc gcc 441  
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ttc agg ctt gag gct gct gcc tgg cct ggc tgg ttc ctg tgt ggc cgc 489  
 Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro  
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gca gag ccc cag cag cca gta cag ctc acc aag gag agt gag ccc tca 537  
 Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser  
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gcc cgt acc aag ttt tac ttt gaa cag agc tgg tag ggagacagga 583  
 Ala Arg Thr Lys Phe Tyr Phe Glu Gln Ser Trp  
 165 170

aactgcgttt tagccttggtg cccccaaacc aagctcatcc tgcctcagggtg ctatggtagg 643

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 35 40 45

Gly Asp Pro Val Ala Asp Asn Cys Cys Ala Glu Lys Ile Cys Ile Leu  
 50 55 60

Pro Asn Arg Gly Leu Ala Arg Thr Lys Val Pro Ile Phe Leu Gly Ile  
 65 70 75 80

Gln Gly Gly Ser Arg Cys Leu Ala Cys Val Glu Thr Glu Glu Gly Pro  
 85 90 95

Ser Leu Gln Leu Glu Asp Val Asn Ile Glu Glu Leu Tyr Lys Gly Gly  
 100 105 110

Glu Glu Ala Thr Arg Phe Thr Phe Phe Gln Ser Ser Ser Gly Ser Ala  
 115 120 125

Phe Arg Leu Glu Ala Ala Ala Trp Pro Gly Trp Phe Leu Cys Gly Pro  
 130 135 140

Ala Glu Pro Gln Gln Pro Val Gln Leu Thr Lys Glu Ser Glu Pro Ser



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Gly Glu Glu Ser Asn Asp Lys Ile Pro Val Ala Leu Gly Leu Lys Glu  
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Lys Asn Leu Tyr Leu Ser Cys Val Leu Lys Asp Lys Pro Thr Leu  
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Gln Leu Glu Ser Val Asp Pro Lys Asn Tyr Pro Lys Lys Lys Met Glu  
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Lys Arg Phe Val Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe  
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Glu Ser Ala Gln Phe Pro Asn Trp Tyr Ile Ser Thr Ser Gln Ala Glu  
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Ser Lys Ile Gln Ala Phe Arg Ile Trp Asp Val Asn Gln Lys Thr Phe



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 Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Tyr Leu Gln Gly Pro Asn  
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     65                                      70                                      75                                      80  
 Leu Phe Leu Gly Ile His Gly Gly Lys Met Cys Leu Ser Cys Val Lys  
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 Asp Ser Gly Pro Thr Thr Ser Phe Glu Ser Ala Ala Cys Pro Gly Trp  
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 Phe Leu Cys Thr Ala Met Glu Ala Asp Gln Pro Val Ser Leu Thr Asn  
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 Ala Gly Lys Val Ile Lys Gly Glu Glu Ile Ser Val Val Pro Asn Arg  
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 Trp Leu Asp Ala Ser Leu Ser Pro Val Ile Leu Gly Val Gln Gly Gly  
     50                                      55                                      60  
 Ser Gln Cys Leu Ser Cys Gly Val Gly Gln Glu Pro Thr Leu Thr Leu  
     65                                      70                                      75                                      80  
 Glu Pro Val Asn Ile Met Glu Leu Tyr Leu Gly Ala Lys Glu Ser Lys  
                                     85                                      90                                      95  
 Ser Phe Thr Phe Tyr Arg Arg Asp Met Gly Leu Thr Ser Ser Phe Glu  
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Ser Ala Ala Tyr Pro Gly Trp Phe Leu Cys Thr Val Pro Glu Ala Asp  
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Gln Pro Val Arg Leu Thr Gln Leu Pro Glu Asn Gly Gly Trp Asn Ala  
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35 40 45

Lys Ile Phe Phe Ala Leu Ala Ser Ser Leu Ser Ser Ala Ser Ala Glu  
50 55 60

Lys Gly Ser Pro Ile Leu Leu Gly Val Ser Lys Gly Glu Phe Cys Leu  
65 70 75 80

Tyr Cys Asp Lys Asp Lys Gly Gln Ser His Pro Ser Leu Gln Leu Lys  
85 90 95

Lys Glu Lys Leu Met Lys Leu Ala Ala Gln Lys Glu Ser Ala Arg Arg  
100 105 110

Pro Phe Ile Phe Tyr Arg Ala Gln Val Gly Ser Trp Asn Met Leu Glu  
115 120 125

Ser Ala Ala His Pro Gly Trp Phe Ile Cys Thr Ser Cys Asn Cys Asn  
130 135 140

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Ser Pro Lys Val Lys Asn Leu Asn Pro Lys Lys Phe Ser Ile His Asp  
50 55 60

Gln Asp His Lys Val Leu Val Leu Asp Ser Gly Asn Leu Ile Ala Val  
65 70 75 80

Pro Asp Lys Asn Tyr Ile Arg Pro Glu Ile Phe Phe Ala Leu Ala Ser  
85 90 95

Ser Leu Ser Ser Ala Ser Ala Glu Lys Gly Ser Pro Ile Leu Leu Gly  
100 105 110

Val Ser Lys Gly Glu Phe Cys Leu Tyr Cys Asp Lys Asp Lys Gly Gln  
115 120 125

Ser His Pro Ser Leu Gln Leu Lys Lys Glu Lys Leu Met Lys Leu Ala  
130 135 140

Ala Gln Lys Glu Ser Ala Arg Arg Pro Phe Ile Phe Tyr Arg Ala Gln  
145 150 155 160

Val Gly Ser Trp Asn Met Leu Glu Ser Ala Ala His Pro Gly Trp Phe  
165 170 175

Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro Val Gly Val Thr Asp Lys  
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Ala Glu Met Ser Pro Ser Glu Val Ser Asp  
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35 40 45

Gly Asn Leu Ile Ala Val Pro Asp Lys Asn Tyr Ile Arg Pro Glu Ile  
50 55 60

Phe Phe Ala Leu Ala Ser Ser Leu Ser Ser Ala Ser Ala Glu Lys Gly  
65 70 75 80

Ser Pro Ile Leu Leu Gly Val Ser Lys Gly Glu Phe Cys Leu Tyr Cys  
85 90 95

Asp Lys Asp Lys Gly Gln Ser His Pro Ser Leu Gln Leu Lys Lys Glu  
100 105 110

Lys Leu Met Lys Leu Ala Ala Gln Lys Glu Ser Ala Arg Arg Pro Phe  
115 120 125

Ile Phe Tyr Arg Ala Gln Val Gly Ser Trp Asn Met Leu Glu Ser Ala  
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Ala His Pro Gly Trp Phe Ile Cys Thr Ser Cys Asn Cys Asn Glu Pro  
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35 40 45

Asp Ser Val Thr Pro Val Thr Val Ala Val Ile Thr Cys Lys Tyr Pro  
50 55 60

Glu Ala Leu Glu Gln Gly Arg Gly Asp Pro Ile Tyr Leu Gly Ile Gln  
65 70 75 80

Asn Pro Glu Met Cys Leu Tyr Cys Glu Lys Val Gly Glu Gln Pro Thr  
85 90 95

Leu Gln Leu Lys Glu Gln Lys Ile Met Asp Leu Tyr Gly Gln Pro Glu  
 100 105 110  
 Pro Val Lys Pro Phe Leu Phe Tyr Arg Ala Lys Thr Gly Arg Thr Ser  
 115 120 125  
 Thr Leu Glu Ser Val Ala Phe Pro Asp Trp Phe Ile Ala Ser Ser Lys  
 130 135 140  
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 Thr Ala Phe Glu Leu Asn Ile Asn Asp  
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 35 40 45  
 Pro Leu Cys Thr Leu Pro Phe Pro Pro Val Cys Lys Pro Ile Thr Gly  
 50 55 60  
 Thr Ile Asn Asp Leu Asn Gln Gln Val Trp Thr Leu Gln Gly Gln Asn  
 65 70 75 80  
 Leu Val Ala Val Pro Arg Ser Asp Ser Val Thr Pro Val Thr Val Ala  
 85 90 95  
 Val Ile Thr Cys Lys Tyr Pro Glu Ala Leu Glu Gln Gly Arg Gly Asp  
 100 105 110  
 Pro Ile Tyr Leu Gly Ile Gln Asn Pro Glu Met Cys Leu Tyr Cys Glu  
 115 120 125  
 Lys Val Gly Glu Gln Pro Thr Leu Gln Leu Lys Glu Gln Lys Ile Met  
 130 135 140  
 Asp Leu Tyr Gly Gln Pro Glu Pro Val Lys Pro Phe Leu Phe Tyr Arg  
 145 150 155 160  
 Ala Lys Thr Gly Arg Thr Ser Thr Leu Glu Ser Val Ala Phe Pro Asp  
 165 170 175  
 Trp Phe Ile Ala Ser Ser Lys Arg Asp Gln Pro Ile Ile Leu Thr Ser

180 185 190  
 Glu Leu Gly Lys Ser Tyr Asn Thr Ala Phe Glu Leu Asn Ile Asn Asp  
 195 200 205

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Val Pro Arg Lys Asp Arg Met Ser Pro Val Thr Ile Ala Leu Ile Ser  
 35 40 45

Cys Arg His Val Glu Thr Leu Glu Lys Asp Arg Gly Asn Pro Ile Tyr  
 50 55 60

Leu Gly Leu Asn Gly Leu Asn Leu Cys Leu Met Cys Ala Lys Val Gly  
 65 70 75 80

Asp Gln Pro Thr Leu Gln Leu Lys Glu Lys Asp Ile Met Asp Leu Tyr  
 85 90 95

Asn Gln Pro Glu Pro Val Lys Ser Phe Leu Phe Tyr His Ser Gln Ser  
 100 105 110

Gly Arg Asn Ser Thr Phe Glu Ser Val Ala Phe Pro Gly Trp Phe Ile  
 115 120 125

Ala Val Ser Ser Glu Gly Gly Cys Pro Leu Ile Leu Thr Gln Glu Leu  
 130 135 140

Gly Lys Ala Asn Thr Thr Asp Phe Gly Leu Thr Met Leu Phe  
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35 40 45

Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu  
50 55 60

Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly  
65 70 75 80

Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val  
85 90 95

Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly  
100 105 110

Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala  
115 120 125

Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly  
130 135 140

Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu  
145 150 155

<210> 18

<211> 11

<212> PRT

<213> Human immunodeficiency virus type 1

<400> 18

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Arg  
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<210> 19

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: internalizing domain derived from HIV tat protein

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<223> Description of Artificial Sequence:

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